

SEQUENCE LISTING

(1) GENERAL INFORMATION:

- (i) APPLICANT: BENOIT, Patrick
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- (ii) TITLE OF INVENTION: MONOCLONAL ANTIBODIES AGAINST THE INTERFERON RECEPTOR, WITH NEUTRALIZING ACTIVITY AGAINST TYPE I INTERFERON
- (iii) NUMBER OF SEQUENCES: 4
- (iv) CORRESPONDENCE ADDRESS:
(A) ADDRESSEE: Foley & Lardner
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(C) CITY: Washington
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- (v) COMPUTER READABLE FORM:
(A) MEDIUM TYPE: Floppy disk
(B) COMPUTER: IBM PC compatible
(C) OPERATING SYSTEM: PC-DOS/MS-DOS
(D) SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
- (vi) CURRENT APPLICATION DATA:
(A) APPLICATION NUMBER: US 08/307,588
(B) FILING DATE: 05-DEC-1994
- C
(vii) PRIOR APPLICATION DATA:
(A) APPLICATION NUMBER: PCT/EP93/00770
(B) FILING DATE: 30-MAR-1993
- (viii) PRIOR APPLICATION DATA:
(A) APPLICATION NUMBER: EP 92400902.0
(B) FILING DATE: 31-MAR-1992
- (ix) ATTORNEY/AGENT INFORMATION:
(A) NAME: SAXE, Bernhard D.
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(C) REFERENCE/DOCKET NUMBER: 17283/117/GUPL
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(2) INFORMATION FOR SEQ ID NO: 1:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1343 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (ix) FEATURE:
(A) NAME/KEY: CDS
(B) LOCATION: 27..1334

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:

CTGCAGGGAT CTGCGGCCGGC TCCCCAG ATG ATG GTC GTC CTC CTG GGC GCG ACG 53
Met Met Val Val Leu Leu Gly Ala Thr
1 5

ACC CTA GTG CTC GTC GCC GTG GGC CCA TGG GTG TTG TCC GCA GCC GCA 101
Thr Leu Val Leu Val Ala Val Gly Pro Trp Val Leu Ser Ala Ala Ala
10 15 20 25

GGT GGA AAA AAT CTA AAA TCT CCT CAA AAA GTA GAG GTC GAC ATC ATA 149
Gly Gly Lys Asn Leu Lys Ser Pro Gln Lys Val Glu Val Asp Ile Ile
30 35 40

GAT GAC AAC TTT ATC CTG AGG TGG AAC AGG AGC GAT GAG TCT GTC GGG 197
Asp Asp Asn Phe Ile Leu Arg Trp Asn Arg Ser Asp Glu Ser Val Gly
45 50 55

AAT GTG ACT TTT TCA TTC GAT TAT CAA AAA ACT GGG ATG GAT AAT TGG 245
Asn Val Thr Phe Ser Phe Asp Tyr Gln Lys Thr Gly Met Asp Asn Trp
60 65 70

ATA AAA TTG TCT GGG TGT CAG AAT ATT ACT AGT ACC AAA TGC AAC TTT 293
Ile Lys Leu Ser Gly Cys Gln Asn Ile Thr Ser Thr Lys Cys Asn Phe
75 80 85

TCT TCA CTC AAG CTG AAT GTT TAT GAA GAA ATT AAA TTG CGT ATA AGA 341
Ser Ser Leu Lys Leu Asn Val Tyr Glu Glu Ile Lys Leu Arg Ile Arg
90 95 100 105

GCA GAA AAA GAA AAC ACT TCT TCA TGG TAT GAG GTT GAC TCA TTT ACA 389
Ala Glu Lys Glu Asn Thr Ser Ser Trp Tyr Glu Val Asp Ser Phe Thr
110 115 120

C'
cont.
CCA TTT CGC AAA GCT CAG ATT GGT CCT CCA GAA GTA CAT TTA GAA GCT 437
Pro Phe Arg Lys Ala Gln Ile Gly Pro Pro Glu Val His Leu Glu Ala
125 130 135

GAA GAT AAG GCA ATA GTG ATA CAC ATC TCT CCT GGA ACA AAA GAT AGT 485
Glu Asp Lys Ala Ile Val Ile His Ile Ser Pro Gly Thr Lys Asp Ser
140 145 150

GTT ATG TGG GCT TTG GAT GGT TTA AGC TTT ACA TAT AGC TTA CTT ATC 533
Val Met Trp Ala Leu Asp Gly Leu Ser Phe Thr Tyr Ser Leu Leu Ile
155 160 165

TGG AAA AAC TCT TCA GGT GTA GAA GAA AGG ATT GAA AAT ATT TAT TCC 581
Trp Lys Asn Ser Ser Gly Val Glu Glu Arg Ile Glu Asn Ile Tyr Ser
170 175 180 185

AGA CAT AAA ATT TAT AAA CTC TCA CCA GAG ACT ACT TAT TGT CTA AAA 629
Arg His Lys Ile Tyr Lys Leu Ser Pro Glu Thr Thr Tyr Cys Leu Lys
190 195 200

GTT AAA GCA GCA CTA CTT ACG TCA TGG AAA ATT GGT GTC TAT AGT CCA 677
Val Lys Ala Ala Leu Leu Thr Ser Trp Lys Ile Gly Val Tyr Ser Pro
205 210 215

GTA CAT TGT ATA AAG ACC ACA GTT GAA AAT GAA CTA CCT CCA CCA GAA 725
Val His Cys Ile Lys Thr Thr Val Glu Asn Glu Leu Pro Pro Pro Glu
220 225 230

AAT ATA GAA GTC AGT GTC CAA AAT CAG AAC TAT GTT CTT AAA TGG GAT 773
Asn Ile Glu Val Ser Val Gln Asn Gln Asn Tyr Val Leu Lys Trp Asp
235 240 245

TAT ACA TAT GCA AAC ATG ACC TTT CAA GTT CAG TGG CTC CAC GCC TTT
Tyr Thr Tyr Ala Asn Met Thr Phe Gln Val Gln Trp Leu His Ala Phe 821
250 255 260 265

TTA AAA AGG AAT CCT GGA AAC CAT TTG TAT AAA TGG AAA CAA ATA CCT
Leu Lys Arg Asn Pro Gly Asn His Leu Tyr Lys Trp Lys Gln Ile Pro 869
270 275 280

GAC TGT GAA AAT GTC AAA ACT ACC CAG TGT GTC TTT CCT CAA AAC GTT
Asp Cys Glu Asn Val Lys Thr Thr Gln Cys Val Phe Pro Gln Asn Val 917
285 290 295

TTC CAA AAA GGA ATT TAC CTT CTC CGC GTA CAA GCA TCT GAT GGA AAT
Phe Gln Lys Gly Ile Tyr Leu Leu Arg Val Gln Ala Ser Asp Gly Asn 965
300 305 310

AAC ACA TCT TTT TGG TCT GAA GAG ATA AAG TTT GAT ACT GAA ATA CAA
Asn Thr Ser Phe Trp Ser Glu Glu Ile Lys Phe Asp Thr Glu Ile Gln 1013
315 320 325

GCT TTC CTA CTT CCT CCA GTC TTT AAC ATT AGA TCC CTT AGT GAT TCA
Ala Phe Leu Leu Pro Pro Val Phe Asn Ile Arg Ser Leu Ser Asp Ser 1061
330 335 340 345

TTC CAT ATC TAT ATC GGT GCT CCA AAA CAG TCT GGA AAC ACG CCT GTG
Phe His Ile Tyr Ile Gly Ala Pro Lys Gln Ser Gly Asn Thr Pro Val 1109
350 355 360

ATC CAG GAT TAT CCA CTG ATT TAT GAA ATT ATT TTT TGG GAA AAC ACT
Ile Gln Asp Tyr Pro Leu Ile Tyr Glu Ile Ile Phe Trp Glu Asn Thr 1157
365 370 375

C
cont.

TCA AAT GCT GAG AGA AAA ATT ATC GAG AAA AAA ACT GAT GTT ACA GTT
Ser Asn Ala Glu Arg Lys Ile Ile Glu Lys Lys Thr Asp Val Thr Val 1205
380 385 390

CCT AAT TTG AAA CCA CTG ACT GTA TAT TGT GTG AAA GCC AGA GCA CAC
Pro Asn Leu Lys Pro Leu Thr Val Tyr Cys Val Lys Ala Arg Ala His 1253
395 400 405

ACC ATG GAT GAA AAG CTG AAT AAA AGC AGT GTT TTT AGT GAC GCT GTA
Thr Met Asp Glu Lys Leu Asn Lys Ser Ser Val Phe Ser Asp Ala Val 1301
410 415 420 425

TGT GAG AAA ACA AAA CCA GGA AAT ACC TCT AAA TGAGGTACC
Cys Glu Lys Thr Lys Pro Gly Asn Thr Ser Lys 1343
430 435

(2) INFORMATION FOR SEQ ID NO: 2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 436 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:

Met Met Val Val Leu Leu Gly Ala Thr Thr Leu Val Leu Val Ala Val
1 5 10 15

Gly Pro Trp Val Leu Ser Ala Ala Gly Gly Lys Asn Leu Lys Ser
20 25 30

Pro Gln Lys Val Glu Val Asp Ile Ile Asp Asp Asn Phe Ile Leu Arg
35 40 45

Trp Asn Arg Ser Asp Glu Ser Val Gly Asn Val Thr Phe Ser Phe Asp
50 55 60

Tyr Gln Lys Thr Gly Met Asp Asn Trp Ile Lys Leu Ser Gly Cys Gln
65 70 75 80

Asn Ile Thr Ser Thr Lys Cys Asn Phe Ser Ser Leu Lys Leu Asn Val
85 90 95

Tyr Glu Glu Ile Lys Leu Arg Ile Arg Ala Glu Lys Glu Asn Thr Ser
100 105 110

Ser Trp Tyr Glu Val Asp Ser Phe Thr Pro Phe Arg Lys Ala Gln Ile
115 120 125

Gly Pro Pro Glu Val His Leu Glu Ala Glu Asp Lys Ala Ile Val Ile
130 135 140

His Ile Ser Pro Gly Thr Lys Asp Ser Val Met Trp Ala Leu Asp Gly
145 150 155 160

Leu Ser Phe Thr Tyr Ser Leu Leu Ile Trp Lys Asn Ser Ser Gly Val
165 170 175

Glu Glu Arg Ile Glu Asn Ile Tyr Ser Arg His Lys Ile Tyr Lys Leu
180 185 190

Ser Pro Glu Thr Thr Tyr Cys Leu Lys Val Lys Ala Ala Leu Leu Thr
195 200 205

Ser Trp Lys Ile Gly Val Tyr Ser Pro Val His Cys Ile Lys Thr Thr
210 215 220

Val Glu Asn Glu Leu Pro Pro Pro Glu Asn Ile Glu Val Ser Val Gln
225 230 235 240

Asn Gln Asn Tyr Val Leu Lys Trp Asp Tyr Thr Tyr Ala Asn Met Thr
245 250 255

Phe Gln Val Gln Trp Leu His Ala Phe Leu Lys Arg Asn Pro Gly Asn
260 265 270

His Leu Tyr Lys Trp Lys Gln Ile Pro Asp Cys Glu Asn Val Lys Thr
275 280 285

Thr Gln Cys Val Phe Pro Gln Asn Val Phe Gln Lys Gly Ile Tyr Leu
290 295 300

Leu Arg Val Gln Ala Ser Asp Gly Asn Asn Thr Ser Phe Trp Ser Glu
305 310 315 320

Glu Ile Lys Phe Asp Thr Glu Ile Gln Ala Phe Leu Leu Pro Pro Val
325 330 335

Phe Asn Ile Arg Ser Leu Ser Asp Ser Phe His Ile Tyr Ile Gly Ala
340 345 350

Pro Lys Gln Ser Gly Asn Thr Pro Val Ile Gln Asp Tyr Pro Leu Ile
355 360 365

Tyr Glu Ile Ile Phe Trp Glu Asn Thr Ser Asn Ala Glu Arg Lys Ile
370 375 380

Ile Glu Lys Lys Thr Asp Val Thr Val Pro Asn Leu Lys Pro Leu Thr
385 390 395 400
Val Tyr Cys Val Lys Ala Arg Ala His Thr Met Asp Glu Lys Leu Asn
405 410 415
Lys Ser Ser Val Phe Ser Asp Ala Val Cys Glu Lys Thr Lys Pro Gly
420 425 430
Asn Thr Ser Lys
435

(2) INFORMATION FOR SEQ ID NO: 3:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1755 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:
(A) NAME/KEY: CDS
(B) LOCATION: 27..1697

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:

CTGCAGGGAT CTGCGGCCGGC TCCCCAG ATG ATG GTC GTC CTC CTG GGC GCG ACG 53
Met Met Val Val Leu Leu Gly Ala Thr
1 5
cont.
ACC CTA GTG CTC GTC GCC GTG GGC CCA TGG GTG TTG TCC GCA GCC GCA 101
Thr Leu Val Leu Val Ala Val Gly Pro Trp Val Leu Ser Ala Ala Ala
10 15 20 25
GGT GGA AAA AAT CTA AAA TCT CCT CAA AAA GTA GAG GTC GAC ATC ATA 149
Gly Gly Lys Asn Leu Lys Ser Pro Gln Lys Val Glu Val Asp Ile Ile
30 35 40
GAT GAC AAC TTT ATC CTG AGG TGG AAC AGG AGC GAT GAG TCT GTC GGG 197
Asp Asp Asn Phe Ile Leu Arg Trp Asn Arg Ser Asp Glu Ser Val Gly
45 50 55
AAT GTG ACT TTT TCA TTC GAT TAT CAA AAA ACT GGG ATG GAT AAT TGG 245
Asn Val Thr Phe Ser Phe Asp Tyr Gln Lys Thr Gly Met Asp Asn Trp
60 65 70
ATA AAA TTG TCT GGG TGT CAG AAT ATT ACT AGT ACC AAA TGC AAC TTT 293
Ile Lys Leu Ser Gly Cys Gln Asn Ile Thr Ser Thr Lys Cys Asn Phe
75 80 85
TCT TCA CTC AAG CTG AAT GTT TAT GAA GAA ATT AAA TTG CGT ATA AGA 341
Ser Ser Leu Lys Leu Asn Val Tyr Glu Glu Ile Lys Leu Arg Ile Arg
90 95 100 105
GCA GAA AAA GAA AAC ACT TCT TCA TGG TAT GAG GTT GAC TCA TTT ACA 389
Ala Glu Lys Glu Asn Thr Ser Ser Trp Tyr Glu Val Asp Ser Phe Thr
110 115 120
CCA TTT CGC AAA GCT CAG ATT GGT CCT CCA GAA GTA CAT TTA GAA GCT 437
Pro Phe Arg Lys Ala Gln Ile Gly Pro Pro Glu Val His Leu Glu Ala
125 130 135

GAA GAT AAG GCA ATA GTG ATA CAC ATC TCT CCT GGA ACA AAA GAT AGT Glu Asp Lys Ala Ile Val Ile His Ile Ser Pro Gly Thr Lys Asp Ser 140 145 150	485
GTT ATG TGG GCT TTG GAT GGT TTA AGC TTT ACA TAT AGC TTA CTT ATC Val Met Trp Ala Leu Asp Gly Leu Ser Phe Thr Tyr Ser Leu Leu Ile 155 160 165	533
TGG AAA AAC TCT TCA GGT GTA GAA GAA AGG ATT GAA AAT ATT TAT TCC Trp Lys Asn Ser Ser Gly Val Glu Arg Ile Glu Asn Ile Tyr Ser 170 175 180 185	581
AGA CAT AAA ATT TAT AAA CTC TCA CCA GAG ACT ACT TAT TGT CTA AAA Arg His Lys Ile Tyr Lys Leu Ser Pro Glu Thr Thr Tyr Cys Leu Lys 190 195 200	629
GTT AAA GCA GCA CTA CTT ACG TCA TGG AAA ATT GGT GTC TAT AGT CCA Val Lys Ala Ala Leu Leu Thr Ser Trp Lys Ile Gly Val Tyr Ser Pro 205 210 215	677
GTA CAT TGT ATA AAG ACC ACA GTT GAA AAT GAA CTA CCT CCA CCA GAA Val His Cys Ile Lys Thr Thr Val Glu Asn Glu Leu Pro Pro Pro Glu 220 225 230	725
AAT ATA GAA GTC AGT GTC CAA AAT CAG AAC TAT GTT CTT AAA TGG GAT Asn Ile Glu Val Ser Val Gln Asn Gln Asn Tyr Val Leu Lys Trp Asp 235 240 245	773
TAT ACA TAT GCA AAC ATG ACC TTT CAA GTT CAG TGG CTC CAC GCC TTT Tyr Thr Tyr Ala Asn Met Thr Phe Gln Val Gln Trp Leu His Ala Phe 250 255 260 265	821
TTA AAA AGG AAT CCT GGA AAC CAT TTG TAT AAA TGG AAA CAA ATA CCT Leu Lys Arg Asn Pro Gly Asn His Leu Tyr Lys Trp Lys Gln Ile Pro 270 275 280	869
GAC TGT GAA AAT GTC AAA ACT ACC CAG TGT GTC TTT CCT CAA AAC GTT Asp Cys Glu Asn Val Lys Thr Thr Gln Cys Val Phe Pro Gln Asn Val 285 290 295	917
TTC CAA AAA GGA ATT TAC CTT CTC CGC GTA CAA GCA TCT GAT GGA AAT Phe Gln Lys Gly Ile Tyr Leu Leu Arg Val Gln Ala Ser Asp Gly Asn 300 305 310	965
AAC ACA TCT TTT TGG TCT GAA GAG ATA AAG TTT GAT ACT GAA ATA CAA Asn Thr Ser Phe Trp Ser Glu Glu Ile Lys Phe Asp Thr Glu Ile Gln 315 320 325	1013
GCT TTC CTA CTT CCT CCA GTC TTT AAC ATT AGA TCC CTT AGT GAT TCA Ala Phe Leu Leu Pro Pro Val Phe Asn Ile Arg Ser Leu Ser Asp Ser 330 335 340 345	1061
TTC CAT ATC TAT ATC GGT GCT CCA AAA CAG TCT GGA AAC ACG CCT GTG Phe His Ile Tyr Ile Gly Ala Pro Lys Gln Ser Gly Asn Thr Pro Val 350 355 360	1109
ATC CAG GAT TAT CCA CTG ATT TAT GAA ATT ATT TTT TGG GAA AAC ACT Ile Gln Asp Tyr Pro Leu Ile Tyr Glu Ile Ile Phe Trp Glu Asn Thr 365 370 375	1157
TCA AAT GCT GAG AGA AAA ATT ATC GAG AAA AAA ACT GAT GTT ACA GTT Ser Asn Ala Glu Arg Lys Ile Ile Glu Lys Lys Thr Asp Val Thr Val 380 385 390	1205
CCT AAT TTG AAA CCA CTG ACT GTA TAT TGT GTG AAA GCC AGA GCA CAC Pro Asn Leu Lys Pro Leu Thr Val Tyr Cys Val Lys Ala Arg Ala His 395 400 405	1253

ACC ATG GAT GAA AAG CTG AAT AAA AGC AGT GTT TTT AGT GAC GCT GTA Thr Met Asp Glu Lys Leu Asn Lys Ser Ser Val Phe Ser Asp Ala Val 410 415 420 425	1301
TGT GAG AAA ACA AAA CCA GGA AAT ACC TCT AAA ATT TGG CTT ATA GTT Cys Glu Lys Thr Lys Pro Gly Asn Thr Ser Lys Ile Trp Leu Ile Val 430 435 440	1349
GGA ATT TGT ATT GCA TTA TTT GCT CTC CCG TTT GTC ATT TAT GCT GCG Gly Ile Cys Ile Ala Leu Phe Ala Leu Pro Phe Val Ile Tyr Ala Ala 445 450 455	1397
AAA GTC TTC TTG AGA TGC ATC AAT TAT GTC TTC TTT CCA TCA CTT AAA Lys Val Phe Leu Arg Cys Ile Asn Tyr Val Phe Phe Pro Ser Leu Lys 460 465 470	1445
CCT TCT TCC AGT ATA GAT GAG TAT TTC TCT GAA CAG CCA TTG AAG AAT Pro Ser Ser Ser Ile Asp Glu Tyr Phe Ser Glu Gln Pro Leu Lys Asn 475 480 485	1493
CTT CTG CTT TCA ACT TCT GAG GAA CAA ATC GAA AAA TGT TTC ATA ATT Leu Leu Leu Ser Thr Ser Glu Glu Gln Ile Glu Lys Cys Phe Ile Ile 490 495 500 505	1541
GAA AAT ATA AGC ACA ATT GCT ACA GTA GAA GAA ACT AAT CAA ACT GAT Glu Asn Ile Ser Thr Ile Ala Thr Val Glu Glu Thr Asn Gln Thr Asp 510 515 520	1589
GAA GAT CAT AAA AAA TAC AGT TCC CAA ACT AGC CAA GAT TCA GGA AAT Glu Asp His Lys Lys Tyr Ser Ser Gln Thr Ser Gln Asp Ser Gly Asn 525 530 535	1637
TAT TCT AAT GAA GAT GAA AGC GAA AGT AAA ACA AGT GAA GAA CTA CAG Tyr Ser Asn Glu Asp Glu Ser Glu Ser Lys Thr Ser Glu Glu Leu Gln 540 545 550	1685
C cont. CAG GAC TTT GTA TGACCAAGAAA TGAACTGTGT CAAGTATAAG GTTTTCAGC Gln Asp Phe Val 555	1737
AGGAGTTACA CTGGTACC	1755

(2) INFORMATION FOR SEQ ID NO: 4:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 557 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:

Met Met Val Val Leu Leu Gly Ala Thr Thr Leu Val Leu Val Ala Val 1 5 10 15
Gly Pro Trp Val Leu Ser Ala Ala Ala Gly Gly Lys Asn Leu Lys Ser 20 25 30
Pro Gln Lys Val Glu Val Asp Ile Ile Asp Asp Asn Phe Ile Leu Arg 35 40 45
Trp Asn Arg Ser Asp Glu Ser Val Gly Asn Val Thr Phe Ser Phe Asp 50 55 60

Tyr Gln Lys Thr Gly Met Asp Asn Trp Ile Lys Leu Ser Gly Cys Gln
65 70 75 80

Asn Ile Thr Ser Thr Lys Cys Asn Phe Ser Ser Leu Lys Leu Asn Val
85 90 95

Tyr Glu Glu Ile Lys Leu Arg Ile Arg Ala Glu Lys Glu Asn Thr Ser
100 105 110

Ser Trp Tyr Glu Val Asp Ser Phe Thr Pro Phe Arg Lys Ala Gln Ile
115 120 125

Gly Pro Pro Glu Val His Leu Glu Ala Glu Asp Lys Ala Ile Val Ile
130 135 140

His Ile Ser Pro Gly Thr Lys Asp Ser Val Met Trp Ala Leu Asp Gly
145 150 155 160

Leu Ser Phe Thr Tyr Ser Leu Leu Ile Trp Lys Asn Ser Ser Gly Val
165 170 175

Glu Glu Arg Ile Glu Asn Ile Tyr Ser Arg His Lys Ile Tyr Lys Leu
180 185 190

Ser Pro Glu Thr Thr Tyr Cys Leu Lys Val Lys Ala Ala Leu Leu Thr
195 200 205

Ser Trp Lys Ile Gly Val Tyr Ser Pro Val His Cys Ile Lys Thr Thr
210 215 220

Val Glu Asn Glu Leu Pro Pro Glu Asn Ile Glu Val Ser Val Gln
225 230 235 240

Asn Gln Asn Tyr Val Leu Lys Trp Asp Tyr Thr Tyr Ala Asn Met Thr
245 250 255

Phe Gln Val Gln Trp Leu His Ala Phe Leu Lys Arg Asn Pro Gly Asn
260 265 270

His Leu Tyr Lys Trp Lys Gln Ile Pro Asp Cys Glu Asn Val Lys Thr
275 280 285

Thr Gln Cys Val Phe Pro Gln Asn Val Phe Gln Lys Gly Ile Tyr Leu
290 295 300

Leu Arg Val Gln Ala Ser Asp Gly Asn Asn Thr Ser Phe Trp Ser Glu
305 310 315 320

Glu Ile Lys Phe Asp Thr Glu Ile Gln Ala Phe Leu Leu Pro Pro Val
325 330 335

Phe Asn Ile Arg Ser Leu Ser Asp Ser Phe His Ile Tyr Ile Gly Ala
340 345 350

Pro Lys Gln Ser Gly Asn Thr Pro Val Ile Gln Asp Tyr Pro Leu Ile
355 360 365

Tyr Glu Ile Ile Phe Trp Glu Asn Thr Ser Asn Ala Glu Arg Lys Ile
370 375 380

Ile Glu Lys Lys Thr Asp Val Thr Val Pro Asn Leu Lys Pro Leu Thr
385 390 395 400

Val Tyr Cys Val Lys Ala Arg Ala His Thr Met Asp Glu Lys Leu Asn
405 410 415

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cont.*

Lys Ser Ser Val Phe Ser Asp Ala Val Cys Glu Lys Thr Lys Pro Gly
420 425 430

Asn Thr Ser Lys Ile Trp Leu Ile Val Gly Ile Cys Ile Ala Leu Phe
435 440 445

Ala Leu Pro Phe Val Ile Tyr Ala Ala Lys Val Phe Leu Arg Cys Ile
450 455 460

Asn Tyr Val Phe Phe Pro Ser Leu Lys Pro Ser Ser Ser Ile Asp Glu
465 470 475 480

Tyr Phe Ser Glu Gln Pro Leu Lys Asn Leu Leu Leu Ser Thr Ser Glu
485 490 495

Glu Gln Ile Glu Lys Cys Phe Ile Ile Glu Asn Ile Ser Thr Ile Ala
500 505 510

Thr Val Glu Glu Thr Asn Gln Thr Asp Glu Asp His Lys Lys Tyr Ser
515 520 525

Ser Gln Thr Ser Gln Asp Ser Gly Asn Tyr Ser Asn Glu Asp Glu Ser
530 535 540

Glu Ser Lys Thr Ser Glu Glu Leu Gln Gln Asp Phe Val
545 550 555

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